



Release 3.1A John F. Collins, Biocomputing Research Unit.
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MPearch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Oct 21 16:29:45 1999; Maspar time 4.57 Seconds
519.801 Million cell updates/sec
No output not generated.

Title: >US-08-978-217-7
Description: (1-84) from US08978217.pep
Perfect Score: 599
Sequence: 1 NCALBELRLVFGPLGDLHA.....ELDDGQOASYPHSGCAG 84

Scoring table:
PAM 150
Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot37
1:swissprot

Statistics: Mean 41.198; Variance 80.907; scale 0.509

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|------------------------------------|-----------|
| 1 | 98 | 16.4 | 174 | 1 | GSPM_PSEAE GENERAL SECRETION PATH | 1.00e+01 |
| 2 | 94 | 15.7 | 277 | 1 | Y021_SYNA3 PUTATIVE PROTEASE SIRO | 3.43e-01 |
| 3 | 94 | 15.7 | 364 | 1 | YBBB_ECOLI HYPOTHETICAL 41.1 KD P | 3.43e-01 |
| 4 | 91 | 15.2 | 958 | 1 | SYAC_YEAST ALANYL-TRNA SYNTHETASE | 8.45e-01 |
| 5 | 91 | 15.2 | 2870 | 1 | NDVB_RHIME 319 KD PROTEIN. | 8.45e-01 |
| 6 | 89 | 14.9 | 395 | 1 | APPA_MOUSE APOLIPROTEIN A-IV PR | 1.52e+00 |
| 7 | 89 | 14.9 | 916 | 1 | SECA_MOUSE PREPROTEIN TRANSLOCASE | 1.52e+00 |
| 8 | 89 | 14.9 | 952 | 1 | IF41_YEAST EUKARYOTIC INITIATION | 1.52e+00 |
| 9 | 88 | 14.7 | 194 | 1 | YFEB_ECOLI HYPOTHETICAL 21.5 KD P | 2.04e+00 |
| 10 | 88 | 14.7 | 241 | 1 | RPEP_ALICEU RIBULOSE-PHOSPHATE 3-E | 2.04e+00 |
| 11 | 88 | 14.7 | 2418 | 1 | SFCA_HUMAN SPECTRIN ALPHA CHAIN, | 2.04e+00 |
| 12 | 86 | 14.4 | 183 | 1 | YDJA_ECOLI HYPOTHETICAL 20.1 KD P | 3.63e+00 |
| 13 | 86 | 14.4 | 308 | 1 | GRP3_ARTSA GLYCINE-RICH PROTEIN G | 3.63e+00 |
| 14 | 86 | 14.4 | 317 | 1 | APE_PIG APOLIPROTEIN E PRECU | 3.63e+00 |
| 15 | 85 | 14.2 | 202 | 1 | SODM_RABIT SUPEROXIDE DISMUTASE [| 4.82e+00 |
| 16 | 85 | 14.2 | 289 | 1 | GLUCOSE-1-PHOSPHATE TH | 4.82e+00 |
| 17 | 85 | 14.2 | 341 | 1 | NUTM_ANOCA MADH-UBIQUINONE OXIDOR | 4.82e+00 |
| 18 | 85 | 14.2 | 341 | 1 | NUTM_ANOCA MADH-UBIQUINONE OXIDOR | 4.82e+00 |
| 19 | 85 | 14.2 | 348 | 1 | NUTM_ANOCA MADH-UBIQUINONE OXIDOR | 4.82e+00 |
| 20 | 85 | 14.2 | 655 | 1 | PARE_BACCU TOPOISOMERASE IV SUBUN | 4.82e+00 |
| 21 | 85 | 14.2 | 785 | 1 | CUL3_SCHRO CULLIN HOMOLOG 3 (CUL- | 4.82e+00 |
| 22 | 85 | 14.2 | 807 | 1 | OXYB_HUMAN OXYSTEROL-BINDING PROT | 4.82e+00 |
| 23 | 85 | 14.2 | 809 | 1 | OXYB_RABIT OXYSTEROL-BINDING PROT | 4.82e+00 |

| | | | | | | |
|----|----|------|------|---|-----------------------------------|----------|
| 24 | 85 | 14.2 | 849 | 1 | FSCI_MOUSE MAJOR FIBROUS SHEATH P | 4.82e+00 |
| 25 | 84 | 14.0 | 187 | 1 | OX4L_RABIT OX40 LIGAND (OX40L). | 6.39e+00 |
| 26 | 84 | 14.0 | 274 | 1 | NUTM_DROMA MADH-UBIQUINONE OXIDOR | 6.39e+00 |
| 27 | 84 | 14.0 | 341 | 1 | NUTM_DROVA MADH-UBIQUINONE OXIDOR | 6.39e+00 |
| 28 | 84 | 14.0 | 341 | 1 | NUTM_DROME MADH-UBIQUINONE OXIDOR | 6.39e+00 |
| 29 | 84 | 14.0 | 351 | 1 | COTS_BACSU SPORE COAT PROTEIN S (| 6.39e+00 |
| 30 | 84 | 14.0 | 942 | 1 | DP01_CHLAU DNA POLYMERASE I (EC 2 | 6.39e+00 |
| 31 | 84 | 14.0 | 1220 | 1 | DDX8_HUMAN PROBABLE ATP-DEPENDENT | 6.39e+00 |
| 32 | 83 | 13.9 | 101 | 1 | YDRH_ECOLI HYPOTHETICAL 11.3 KD P | 8.44e+00 |
| 33 | 83 | 13.9 | 249 | 1 | EIA_ADEAL EARLY FIA 27 KD PROTEI | 8.44e+00 |
| 34 | 83 | 13.9 | 868 | 1 | NIB0_YEAST NIP80 PROTEIN (NIP100 | 8.44e+00 |
| 35 | 83 | 13.9 | 896 | 1 | EP15_HUMAN EPIDERMAL GROWTH FACTO | 8.44e+00 |
| 36 | 83 | 13.9 | 1469 | 1 | DP27_CAEL CHROMOSOME CONDENSATIO | 8.44e+00 |
| 37 | 82 | 13.7 | 166 | 1 | VG17_BPH2 EARLY PROTEIN GP17. | 1.11e+01 |
| 38 | 82 | 13.7 | 222 | 1 | SODM_HUMAN SUPEROXIDE DISMUTASE [| 1.11e+01 |
| 39 | 82 | 13.7 | 222 | 1 | SODM_MOUSE SUPEROXIDE DISMUTASE [| 1.11e+01 |
| 40 | 82 | 13.7 | 274 | 1 | NUTM_DROSE MADH-UBIQUINONE OXIDOR | 1.11e+01 |
| 41 | 82 | 13.7 | 274 | 1 | NUTM_DROSI MADH-UBIQUINONE OXIDOR | 1.11e+01 |
| 42 | 82 | 13.7 | 568 | 1 | MEND_HAEIN 2-SUCCINYL-6-HYDROXY-2 | 1.11e+01 |
| 43 | 82 | 13.7 | 658 | 1 | SPEA_ECOLI BIOSYNTHETIC ARGININE | 1.11e+01 |
| 44 | 82 | 13.7 | 864 | 1 | ALKS_PSEOL REGULATORY PROTEIN ALK | 1.11e+01 |
| 45 | 82 | 13.7 | 1168 | 1 | DDX8_SCHPO PUTATIVE PRE-MRNA SPLI | 1.11e+01 |

ALIGNMENTS

RESULT 1
ID GSPM_PSEAE STANDARD: PRT: 174 AA.

AC P25061;
DT 01-MAY-1992 (REL. 22, CREATED)
DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE GENERAL SECRETION PATHWAY PROTEIN M.

GN XCPZ.
OS PSEUDOMONAS AERUGINOSA.
OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; PSEUDOMONAS GROUP;
OC PSEUDOMONAS.

RP SEQUENCE FROM N.A.
RX MEDLINE: 91092255.
RA FILLOUX A., BALLY M., BALL G., AKRIM M., TOMMASSEN J., LAZDUNSKI A.;
RT "Protein secretion in gram-negative bacteria: transport across the
RT outer membrane involves common mechanisms in different bacteria.";
RL EMBL J. 9:4323-4329(1990).

CC -1- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE
CC EXPORT OF PROTEINS.
CC -1- SUBCELLULAR LOCATION: INNER MEMBRANE (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE EXEM/PUTM/OUTM/XCPZ FAMILY.

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CC EMBL: X56183; G45443; -
DR PIR: S12356; S12356.
DR PIR: S21639; S21639.
KW TRANSPORT; TRANSMEMBRANE; INNER MEMBRANE.
FT TRANSMEM
SQ SEQUENCE 174 AA: 19265 MW: 2160888F CRC32:

Query Match 16.4%; Score 98; DB 1; Length 174;
Best local Similarity 30.4%; Pred. No. 1.00e-01;
Matches 17; Conservative 17; Mismatches 21; Indels 1; Gaps 1;

Db 98 ALQGWNTASAAQAGSVERLDNGBGCAVOVALQAPFAFLRLWLDQNGCQVQA 153
OY 20 AQLRDLTSSSSDELSTWIELLEKDM-AFOEALDPGFDGSPFAOELLDDGQAS 74